16. A method of claim 1, 5, 6, 7, 8 or 15 wherein the method of detecting the methylation is a method using methylation sensitive restriction enzyme, a method using chemical modification by hydrazine, permanganic acids or sodium bisulfite, an immunological method using antibodies specific to methylated DNA, affinity column method or DGGE (denaturing gradient gel electrophoresis) method.

IN THE ABSTRACT:

Please substitute the attached abstract, which commences on a separate sheet, for that which was originally filed.

REMARKS

With entry of this amendment, claims 1 and 5-29 are pending. The claims have been amended to overcome 35 USC § 112, first and second paragraph rejections, and to correct informalities. No new matter has been added. Reconsideration is requested.

The Examiner objected to the abstract and claims as not commencing on a separate sheet. Copies of the claims and abstract on separate pages are filed herewith.

Claims 1, 2, and 15 were rejected under 35 U.S.C. 112, first paragraph, as being overly broad. Claim 2 has been cancelled, and Claim 1 amended to change "cell-proliferating disease" to "Psoriasis", and "cytokine receptor gene" to "epidermal growth factor receptor gene". Claim 15 has been amended to change "cytokine receptor gene" to "epidermal growth factor receptor gene". It is respectfully submitted that the amended claims are free of the rejection. Reconsideration and withdrawal are respectfully requested.

The Examiner has rejected claims 1, 3, 6 and 7 under 35 USC § 112, second paragraph, as being indefinite, as set forth on pages 6-8 of the Action. The claims have been amended as follows and are believed to be free of the rejection.

Regarding (a.), additional method steps have been added to Claim 1, as helpfully suggested by the Examiner. It is respectfully submitted that this portion of the rejection has been overcome.

Regarding (b.), Claim 3 has been cancelled, thereby rendering this portion of the rejection moot.

Regarding (c.), Claim 1 has been amended to provide proper antecedent basis for claim 6. It is respectfully submitted that this portion of the rejection has been overcome.

Regarding (d.), Applicants have adopted the Examiner's helpful suggestion and have amended Claim 7 to clarify that the 668th, 671th, 687th and 697th amino acid residue described in Seq. ID No. 4 are cytosines. It is respectfully submitted that this portion of the rejection has been overcome.

In view of these amendments, reconsideration and withdrawal of the 35 USC § 112, second paragraph rejection is respectfully requested.

Claims 1-5, 15, and 16 were rejected under 35 USC § 102(b) as being anticipated by Gamou in light of Kaneko et al. Applicants have amended Claim 1, and cancelled Claims 2, 3 and 4. It is respectfully submitted that the claims are not anticipated for the following reasons.

Gamou discloses a method for determining the methylation level of cytosine residues of the regulatory region by isolating EGFR genes from lung carcinoma derived cells. In contrast, Claims 1 and 5 recite a diagnostic method for detecting psoriasis, and not a diagnostic method for detecting lung carcinoma. There is no disclosure or suggestion in the prior art of the method recited in Claims 1 and 5, and therefore, it is respectfully submitted that Claims 1 and 5 are novel.

Further, the present invention relates to a method of determining the methylation level of cytosine residue by isolating the genome from blood extracted from a sample. Collecting cells from a patient involves pain, however, collecting blood is simple and easy, and therefore, it is certain to be able to collect. The cited art does not disclose or suggest the collection of sample in the diagnostic method. Therefore, Applicants respectfully submit that the method recited in Claims 15 and 16 is novel and non-obvious.

For all of these reasons, withdrawal of the rejection under 35 USC § 102(b) is respectfully requested.

Claim 6 has been rejected under 35 USC § 103(a) as being unpatentable over Gamou in view of Ishii et al. in further view of Johnson. This rejection is traversed for the following reasons.

The Examiner has taken the position that in the prior art of Ishii et al., base sequence analysis of EGFR is conducted to find the CCGG motif which is thought to be a DNA methylation site, and the Seq. ID No. 4 described in the present description is a fraction that corresponds to GenBank Accession Number M 38425. According to the Examiner, it is known to the person skilled in the art of the present field, and that therefore, the present invention would be obvious by applying the method of Gamou as described previously. Applicants respectfully disagree.

The present invention refers to a diagnostic method of psoriasis, focused on the methylation of cytosine residue as described above. However, there is no disclosure or suggestion regarding the application of diagnosis of psoriasis in any of the cited arts. Therefore, Applicants respectfully submit that the present invention would not be achieved even if the cited arts were combined. For these reasons, withdrawal of the 35 USC § 103 rejection is respectfully requested.

Applicants appreciate the Examiner's indication that Claims 7 and 8 are free of the prior art, and would be allowable if properly written in independent form. Applicants believe that all of the claims are patentable, and will accordingly defer such amendment at this time.

All objections and rejections having been addressed, it is respectfully submitted that the application is in condition for allowance, and Notice to that effect is respectfully requested.

Respectfully submitted,

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APPENDIX

Claims as amended:

1[,]. A diagnostic method for detecting [cell-proliferating diseases characterized by] psoriasis which comprises;
collecting a genomic DNA from each sample of psoriasis patients,
amplifying the genomic DNA by using primers in accordance with PCR method,
determining the methylation [level] of cytosine residue(s) at the specific region of epidermal growth factor receptor and,
detecting a psoriasis patient whose sample's genomic [genome] DNA [involved in the expression of cytokine receptor gene] has less cytosine residues than healthy person's genomic DNA.

5[,]. A diagnostic method [in] of claim 1 wherein the specific region is a region in CpG island of promoter or intron.

6[,]. A diagnostic method [in] of claim 1 wherein the specific region is a region involved in the expression of epidermal growth factor receptor gene and a region represented by the nucleotide sequence from 381st position to 962nd position in the nucleotide sequence as described in Seq. ID No. 4.

7[,]. A diagnostic method [in] of claim [6] 1 characterized by determining the methylation of cytosine [level] of [668th] residue 668, [671st] residue 671, [687th] residue 687 and [697th] residue 697 [cytosine-residues] in the nucleotide sequence as described in Seq. ID No. 4.

8[,]. A diagnostic method [in] of claim [7] 1 characterized by [analyzing] determining the methylation of cytosine-residues [level] of 668th [cytosine-residues] in the nucleotide sequence as described in Seq. ID No. 4.

11[,]. A diagnostic method [in] of claim 10 characterized by determining the level of methylation of 268th, 276th and 288th cytosine residues in the nucleotide sequence as described in Seq. ID No. 8.

12[,]. A diagnostic method [in] of claim 11 characterized by analyzing the level of methylation of 268th cytosine residue in the nucleotide sequence as described in Seq. ID No. 8.

15[,]. A method of detecting the [level of] methylation of cytosine residue(s) in the specific region of DNA involved in the expression of [cytokine receptor] epidermal growth factor receptor gene isolated sampling-blood.

16[,]. A method [in] of claim 1, 5, 6, 7, 8 or 15 wherein the method of detecting the [level of] methylation is a method using methylation sensitive restriction enzyme, a method using chemical modification by hydrazine, permanganic acids or sodium bisulfite, an immunological method using antibodies specific to methylated DNA, affinity column method or DGGE (denaturing gradient gel electrophoresis) method.